

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/308,397

DATE: 03/22/2000
TIME: 10:42:16

Input Set: I308397.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Gentry, Daniel R.
2 Lonsdale, John T.
3 Payne, David J.
4 Pearson, Stewart C.
5 Van Aller, Glenn
6 <120> TITLE OF INVENTION: Novel FabD
7 <130> FILE REFERENCE: P50593
8 <140> CURRENT APPLICATION NUMBER: US/09/308,397
9 <141> CURRENT FILING DATE: 1999-05-18
10 <150> EARLIER APPLICATION NUMBER: US 60/031,160
11 <151> EARLIER FILING DATE: 1996-11-18
12 <150> EARLIER APPLICATION NUMBER: PCT/US97/20992
13 <151> EARLIER FILING DATE: 1997-11-14
14 <160> NUMBER OF SEQ ID NOS: 6
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
16 <210> SEQ ID NO 1
17 <211> LENGTH: 921
18 <212> TYPE: DNA
19 <213> ORGANISM: Streptococcus pneumoniae
20 <400> SEQUENCE: 1
21 atgactaaaa cagccttttt atttgctggt caaggtgccc agtatctagg gatgggacgg 60
22 gattttctatg atcagtatcc gattgtcaaa gaaacgattg atcgagcgag tcaggtgctc 120
23 ggttatgatt tacgttatct catcgatacg gaagaagaca aactcaatca gaccgcgtat 180
24 acgcaaccag ccattctagc gacttcgggt gctatctacc gtttattgca agaaaagggc 240
25 tatcagcctg atatggttgc tggtttgtct cttggagaat actctgcctt ggtggcaagc 300
26 ggcgccttgg attttgaaga tgcggttgcc ttggtagcta agcgtggagc ctatatggaa 360
27 gaagcggctc ctgctgactc tggcaagatg gtagcagttc tcaatacgcc agtagaggtc 420
28 attgaagaag cctgtcaaaa agcttctgaa cttggagtgg ttactccagc caactataac 480
29 acacctgcac aaatcgatc tgctggagaa gtggttgagc ttgatcgagc ggttgaactt 540
30 ttgcaagaag caggtgcaa acgcttgatt cctcttaagg tgtcaggtcc ctttcacacc 600
31 gctctccttg agcctgctag ccagaaacta gctgaaactc tagctcaggt aagtttttca 660
32 gattttactt gtcccctagt cggcaatata gaagctgctg tgatgcaaaa agaggacatt 720
33 gctcagctct tgacgcgtca ggtcaaggaa cccgttcggt tctatgaaag tattgggggtc 780
34 atgcaagaag caggcataag caactttatc gagattggac cggggaaagt cttgtcaggt 840
35 tttgttaaaa aaattgatca aactgctcac ttagctcatg tggaagatca agcgagtta 900
36 gtagcacttt tagaaaaata g 921
37 <210> SEQ ID NO 2
38 <211> LENGTH: 306
39 <212> TYPE: PRT
40 <213> ORGANISM: Streptococcus pneumoniae
41 <400> SEQUENCE: 2
42 Met Thr Lys Thr Ala Phe Leu Phe Ala Gly Gln Gly Ala Gln Tyr Leu
43 1 5 10 15
44 Gly Met Gly Arg Asp Phe Tyr Asp Gln Tyr Pro Ile Val Lys Glu Thr

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PAGE: 2

RAW SEQUENCE LISTING
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|----|-----|-----|-----|-----|-----|-----|-----|
| 45 | | 20 | | 25 | | 30 | |
| 46 | Ile | Asp | Arg | Ala | Ser | Gln | Val |
| 47 | | 35 | | 40 | | 45 | |
| 48 | Asp | Thr | Glu | Glu | Asp | Lys | Leu |
| 49 | | 50 | | 55 | | 60 | |
| 50 | Ile | Leu | Ala | Thr | Ser | Val | Ala |
| 51 | 65 | | | 70 | | 75 | |
| 52 | Tyr | Gln | Pro | Asp | Met | Val | Ala |
| 53 | | | | 85 | | 90 | |
| 54 | Leu | Val | Ala | Ser | Gly | Ala | Leu |
| 55 | | | | 100 | | 105 | |
| 56 | Ala | Lys | Arg | Gly | Ala | Tyr | Met |
| 57 | | | | 115 | | 120 | |
| 58 | Lys | Met | Val | Ala | Val | Leu | Asn |
| 59 | | | | 130 | | 135 | |
| 60 | Cys | Gln | Lys | Ala | Ser | Glu | Leu |
| 61 | 145 | | | 150 | | 155 | |
| 62 | Thr | Pro | Ala | Gln | Ile | Val | Ile |
| 63 | | | | 165 | | 170 | |
| 64 | Ala | Val | Glu | Leu | Leu | Gln | Glu |
| 65 | | | | 180 | | 185 | |
| 66 | Lys | Val | Ser | Gly | Pro | Phe | His |
| 67 | | | | 195 | | 200 | |
| 68 | Lys | Leu | Ala | Glu | Thr | Leu | Ala |
| 69 | | | | 210 | | 215 | |
| 70 | Pro | Leu | Val | Gly | Asn | Thr | Glu |
| 71 | 225 | | | 230 | | 235 | |
| 72 | Ala | Gln | Leu | Leu | Thr | Arg | Gln |
| 73 | | | | 245 | | 250 | |
| 74 | Ser | Ile | Gly | Val | Met | Gln | Glu |
| 75 | | | | 260 | | 265 | |
| 76 | Gly | Pro | Gly | Lys | Val | Leu | Ser |
| 77 | | | | 275 | | 280 | |
| 78 | Ala | His | Leu | Ala | His | Val | Glu |
| 79 | | | | 290 | | 295 | |
| 80 | Glu | Lys | | | | | |
| 81 | | | | 305 | | | |

82 <210> SEQ ID NO 3
83 <211> LENGTH: 450
84 <212> TYPE: DNA
85 <213> ORGANISM: Streptococcus pneumoniae
86 <400> SEQUENCE: 3
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88 ctcgctgggc aggagttgta agaaatgact aaaacagcct ttttatttgc tgggtcaagg 120
89 gccagtatc tagggatggg acgggatttc tatgatcagt atccgattgt caaagaaacg 180
90 attgatcgag cgagtcaggt gctcggttat gatttacgtt atctcatcga tacggaagaa 240
91 gacaaactca atcagaccgc ctatacgcaa ccagccattc tagcgacttc ggttgctatc 300
92 taccgtttat tgcaagaaaa gggctatcag cctgatattg ttgctgggtt gtctcttgga 360
93 gaataactctg ccttggtggc aagcggcgcc ttggattttg aagatgcggt tgccttgga 420
94 gctaagcgtg ggcctatat ggaagaagcg 450

11:51:17
03/22/2000
10:42:16

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/308,397

DATE: 03/22/2000

TIME: 10:42:16

Input Set: I308397.RAW

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95 <210> SEQ ID NO 4
96 <211> LENGTH: 122
97 <212> TYPE: PRT
98 <213> ORGANISM: Streptococcus pneumoniae
99 <400> SEQUENCE: 4
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101      1          5          10          15
102 Gly Met Gly Arg Asp Phe Tyr Asp Gln Tyr Pro Ile Val Lys Glu Thr
103      20          25          30
104 Ile Asp Arg Ala Ser Gln Val Leu Gly Tyr Asp Leu Arg Tyr Leu Ile
105      35          40          45
106 Asp Thr Glu Glu Asp Lys Leu Asn Gln Thr Arg Tyr Thr Gln Pro Ala
107      50          55          60
108 Ile Leu Ala Thr Ser Val Ala Ile Tyr Arg Leu Leu Gln Glu Lys Gly
109      65          70          75          80
110 Tyr Gln Pro Asp Met Val Ala Gly Leu Ser Leu Gly Glu Tyr Ser Ala
111      85          90          95
112 Leu Val Ala Ser Gly Ala Leu Asp Phe Glu Asp Ala Val Ala Leu Val
113      100         105         110
114 Ala Lys Arg Gly Ala Tyr Met Glu Glu Ala
115      115         120
116 <210> SEQ ID NO 5
117 <211> LENGTH: 547
118 <212> TYPE: DNA
119 <213> ORGANISM: Streptococcus pneumoniae
120 <400> SEQUENCE: 5
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122 ctgtcaaaag cttctggaac ttggagtggg tactccagcc aactataaca cacctgcaca      120
123 aatcgtcatt gctggagaag tgggtgcagt tgatcgagcg gttgaacttt tgcaagaagc      180
124 aggtgcaaaa cgcttgattc ctcttaaggt gtcaggtccc tttcacaccg ctctccttga      240
125 gctgtctagc cagaaactag ctgaaactct agctcaggtg agtttttcag attttacttg      300
126 tcccctagtc ggcaatacag aagctgctgt gatgcaaaaa gaggacattg ctcagctctt      360
127 gacgcgtcag gtcaaggaac ccgttcggtt ctatgaaagt attgggggtca tgcaagaagc      420
128 aggcataagc aacttattcg agattggacc ggggaaagtc ttgtcaggtt ttgttaaaaa      480
129 aattgatcaa actgctcact tagctcatgt ggaagatcaa gcgagtttag tagcactttt      540
130 agaaaaa      547
131 <210> SEQ ID NO 6
132 <211> LENGTH: 182
133 <212> TYPE: PRT
134 <213> ORGANISM: Streptococcus pneumoniae
135 <400> SEQUENCE: 6
136 Ala Glu Leu Gly Lys Met Val Ala Val Leu Asn Thr Pro Val Glu Val
137      1          5          10          15
138 Ile Glu Glu Ala Cys Gln Lys Leu Leu Glu Leu Gly Val Val Thr Pro
139      20          25          30
140 Ala Asn Tyr Asn Thr Pro Ala Gln Ile Val Ile Ala Gly Glu Val Val
141      35          40          45
142 Ala Val Asp Arg Ala Val Glu Leu Leu Gln Glu Ala Gly Ala Lys Arg
143      50          55          60
144 Leu Ile Pro Leu Lys Val Ser Gly Pro Phe His Thr Ala Leu Leu Glu

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PAGE: 4

RAW SEQUENCE LISTING
 PATENT APPLICATION US/09/308,397

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Input Set: I308397.RAW

| | | | | |
|-----|---|-----|-----|-----|
| 145 | 65 | 70 | 75 | 80 |
| 146 | Pro Ala Ser Gln Lys Leu Ala Glu Thr Leu Ala Gln Val Ser Phe Ser | | | |
| 147 | | 85 | 90 | 95 |
| 148 | Asp Phe Thr Cys Pro Leu Val Gly Asn Thr Glu Ala Ala Val Met Gln | | | |
| 149 | | 100 | 105 | 110 |
| 150 | Lys Glu Asp Ile Ala Gln Leu Leu Thr Arg Gln Val Lys Glu Pro Val | | | |
| 151 | | 115 | 120 | 125 |
| 152 | Arg Phe Tyr Glu Ser Ile Gly Val Met Gln Glu Ala Gly Ile Ser Asn | | | |
| 153 | | 130 | 135 | 140 |
| 154 | Leu Phe Glu Ile Gly Pro Gly Lys Val Leu Ser Gly Phe Val Lys Lys | | | |
| 155 | | 145 | 150 | 155 |
| 156 | Ile Asp Gln Thr Ala His Leu Ala His Val Glu Asp Gln Ala Ser Leu | | | |
| 157 | | 165 | 170 | 175 |
| 158 | Val Ala Leu Leu Glu Lys | | | |
| 159 | | 180 | | |

PAGE: 5

VERIFICATION SUMMARY
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Line ? Error/Warning

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